Hepatoprotective effects of systemic ER activation

ChIPseq/Epigenome genome - Differential binding analysis

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```
library(tidyverse)
library(DiffBind)
```

```
sessionInfo()
```

```
## R version 4.2.3 (2023-03-15)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur ... 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] DiffBind_3.8.4              SummarizedExperiment_1.28.0
##  [3] Biobase_2.58.0              MatrixGenerics_1.10.0
##  [5] matrixStats_1.0.0           GenomicRanges_1.50.2
##  [7] GenomeInfoDb_1.34.9         IRanges_2.32.0
##  [9] S4Vectors_0.36.2            BiocGenerics_0.44.0
## [11] lubridate_1.9.2             forcats_1.0.0
## [13] stringr_1.5.0               dplyr_1.1.2
## [15] purrr_1.0.2                 readr_2.1.4
## [17] tidyr_1.3.0                 tibble_3.2.1
## [19] ggplot2_3.4.3               tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] bitops_1.0-7            RColorBrewer_1.1-3      numDeriv_2016.8-1.1
##  [4] tools_4.2.3             irlba_2.3.5.1           utf8_1.2.3
##  [7] R6_2.5.1                KernSmooth_2.23-20      DBI_1.1.3
## [10] colorspace_2.1-0        apeglm_1.20.0           withr_2.5.0
## [13] tidyselect_1.2.0        compiler_4.2.3          cli_3.6.1
## [16] DelayedArray_0.24.0     rtracklayer_1.58.0      caTools_1.18.2
```

```
## [19] scales_1.2.1            SQUAREM_2021.1          mvtnorm_1.2-2
## [22] mixsqp_0.3-48           digest_0.6.33           Rsamtools_2.14.0
## [25] rmarkdown_2.23          XVector_0.38.0          jpeg_0.1-10
## [28] pkgconfig_2.0.3         htmltools_0.5.5         BSgenome_1.66.3
## [31] invgamma_1.1            fastmap_1.1.1           bbmle_1.0.25
## [34] limma_3.54.2            htmlwidgets_1.6.2       rlang_1.1.1
## [37] rstudioapi_0.15.0       BiocIO_1.8.0            generics_0.1.3
## [40] hwriter_1.3.2.1         BiocParallel_1.32.6     gtools_3.9.4
## [43] RCurl_1.98-1.12         magrittr_2.0.3          GenomeInfoDbData_1.2.9
## [46] interp_1.1-4            Matrix_1.5-3            Rcpp_1.0.11
## [49] munsell_0.5.0           fansi_1.0.4             lifecycle_1.0.3
## [52] stringi_1.7.12          yaml_2.3.7              MASS_7.3-58.2
## [55] zlibbioc_1.44.0         plyr_1.8.8              gplots_3.1.3
## [58] grid_4.2.3              parallel_4.2.3          ggrepel_0.9.3
## [61] bdsmatrix_1.3-6         crayon_1.5.2            deldir_1.0-9
## [64] lattice_0.20-45         Biostrings_2.66.0       hms_1.1.3
## [67] locfit_1.5-9.8          knitr_1.43              pillar_1.9.0
## [70] rjson_0.2.21            systemPipeR_2.4.0       codetools_0.2-19
## [73] XML_3.99-0.14           glue_1.6.2              evaluate_0.21
## [76] ShortRead_1.56.1        GreyListChIP_1.30.0     latticeExtra_0.6-30
## [79] png_0.1-8               vctrs_0.6.3             tzdb_0.4.0
## [82] gtable_0.3.3            amap_0.8-19             ashr_2.2-54
## [85] emdbook_1.3.13          xfun_0.39               restfulr_0.0.15
## [88] coda_0.19-4             truncnorm_1.0-9         GenomicAlignments_1.34.1
## [91] timechange_0.2.0
```

```
getwd()
```

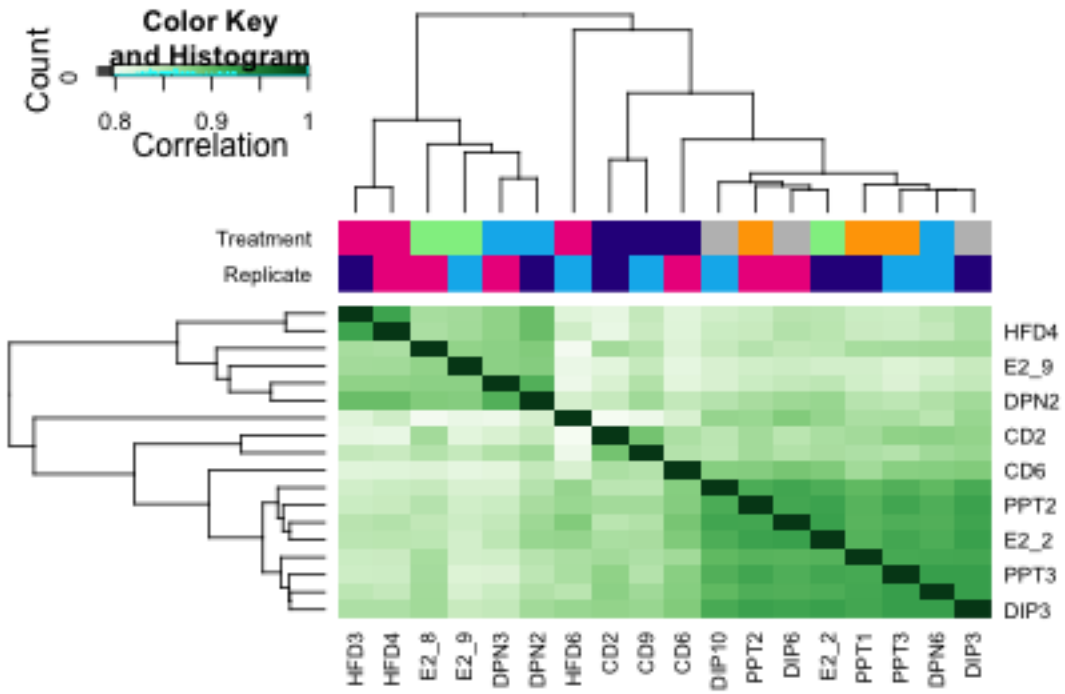
```
## [1] "/Users/christiansom/Documents/GitHub/MAFLD_ER_agonists"
```

```
samples <- c("CD2","CD6", "CD9", "HFD3", "HFD4","HFD6", "DPN2", "DPN3","DPN6","DIP3", "DIP6","DIP10", "
Factor_K27 <- c(rep("H3K27ac", 18))
PeakCaller <- c(rep("macs", 18))
Replicate <- c(rep(1:3, 6))
Treatment <- c(rep("CD", 3), rep("HFD", 3), rep("DPN", 3), rep("DIP", 3), rep("E2", 3), rep("PPT", 3))
files_K27 <- c("data/files/Peak_calling_MACS2/231128_CK0744_H3K27ac_CD2_peaks.broadPeak",
               "data/files/Peak_calling_MACS2/231128_CD6_H3K27ac_peaks.broadPeak",
               "data/files/Peak_calling_MACS2/231128_CK0745_H3K27ac_CD9_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_CK0746_H3K27ac_HFD3_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_CK0747_H3K27ac_HFD4_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_HFD6_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_CK0748_H3K27ac_DPN2_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_CK0749_H3K27ac_DPN3_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_DPN6_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_DIP3_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_DIP6_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_DIP10_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_E2_2_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_CK0750_H3K27ac_E2_8_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_CK0751_H3K27ac_E2_9_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_PPT1_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_PPT2_H3K27ac_peaks.broadPeak",
           "data/files/Peak_calling_MACS2/231128_PPT3_H3K27ac_peaks.broadPeak")
```

```
bam.files_K27 <- c("data/files/BAMdata/H3K27ac/231127_CK0744_H3K27ac_CD2_psort_BL_fix_MkDup.bam",
                   "data/files/BAMdata/H3K27ac/231127_CD6_H3K27ac_S2_R1_001_psort_BL_fix_MkDup.bam",
                   "data/files/BAMdata/H3K27ac/231127_CK0745_H3K27ac_CD9_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_CK0746_H3K27ac_HFD3_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_CK0747_H3K27ac_HFD4_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_HFD6_H3K27ac_S8_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_CK0748_H3K27ac_DPN2_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_CK0749_H3K27ac_DPN3_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_DPN6_H3K27ac_S15_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_DIP3_H3K27ac_S9_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_DIP6_H3K27ac_S10_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_DIP10_H3K27ac_S11_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_E2_2_H3K27ac_S16_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_CK0750_H3K27ac_E2_8_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_CK0751_H3K27ac_E2_9_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_PPT1_H3K27ac_S12_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_PPT2_H3K27ac_S13_R1_001_psort_BL_fix_MkDup.bam",
                "data/files/BAMdata/H3K27ac/231127_PPT3_H3K27ac_S14_R1_001_psort_BL_fix_MkDup.bam")

metaData_K27 <- data.frame(SampleID = samples, Factor = Factor_K27, Replicate = Replicate, Peaks = files
samplesheet_K27 <- dba(sampleSheet=metaData_K27)
```

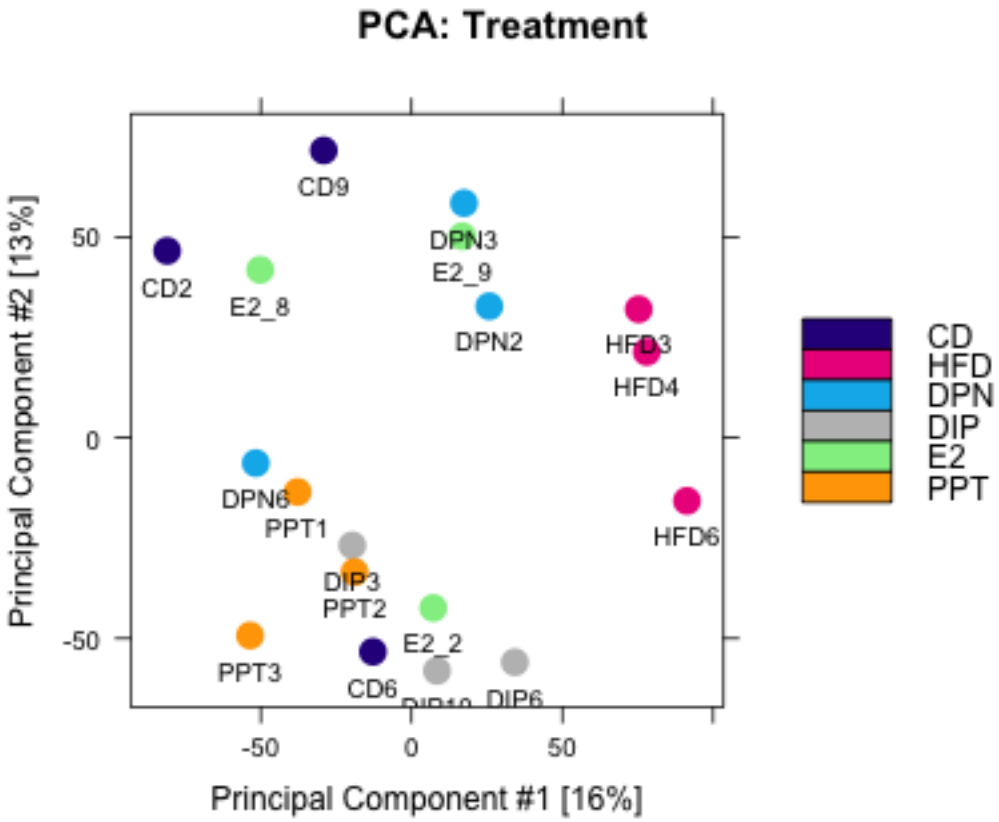
```
dba.plotHeatmap(samplesheet_K27)
```



```
samplesheet.counted_K27 <- dba.count(samplesheet_K27, minOverlap = 2)
dba.overlap(samplesheet_K27,mode=DBA_OLAP_RATE)
```

```
##  [1] 77016 59463 52812 48728 45735 43432 41480 39805 38306 36957 35662 34403
## [13] 33159 31930 30615 29154 27484 25079
```

```
#That is a PCA based on read counts
dba.plotPCA(samplesheet.counted_K27, label=DBA_ID)
```



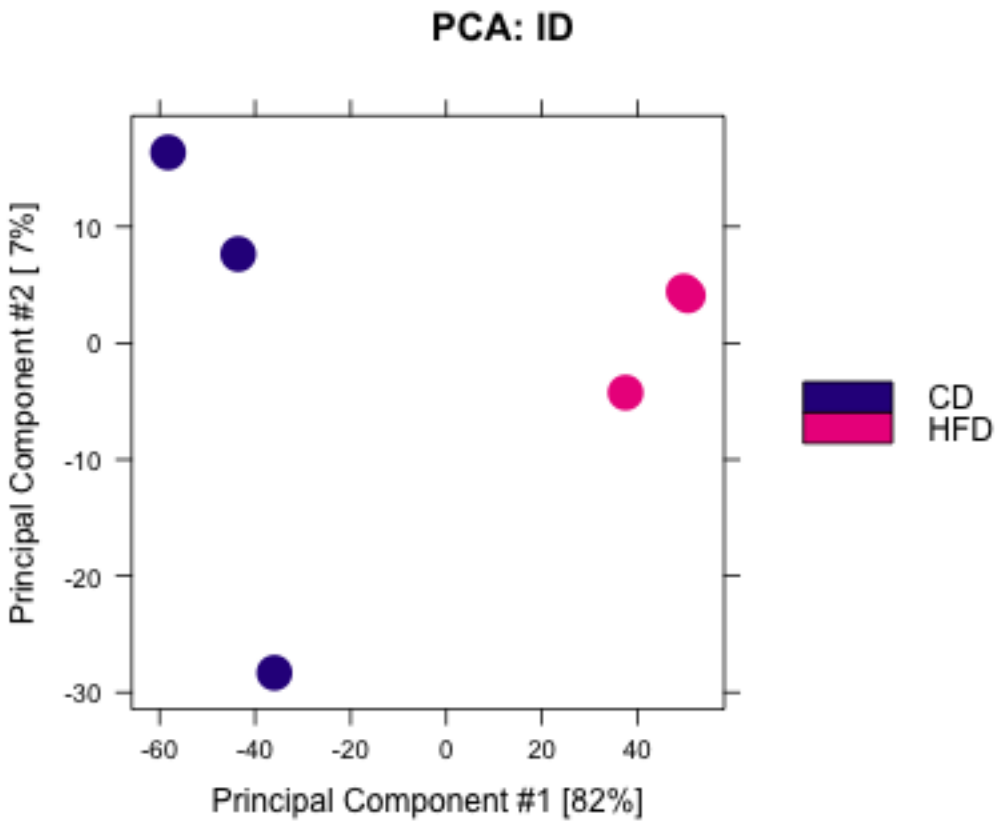

```
contrasts_K27 <- dba.contrast(samplesheet.counted_K27, categories=c(DBA_TREATMENT), minMembers=2)
samplesheet.analysed_K27 <- dba.analyze(contrasts_K27)
```

```
#That is a PCA based on diffbound sites of given contrast
##Get contrast numbers
dba.show(samplesheet.analysed_K27, bContrast=T)
```

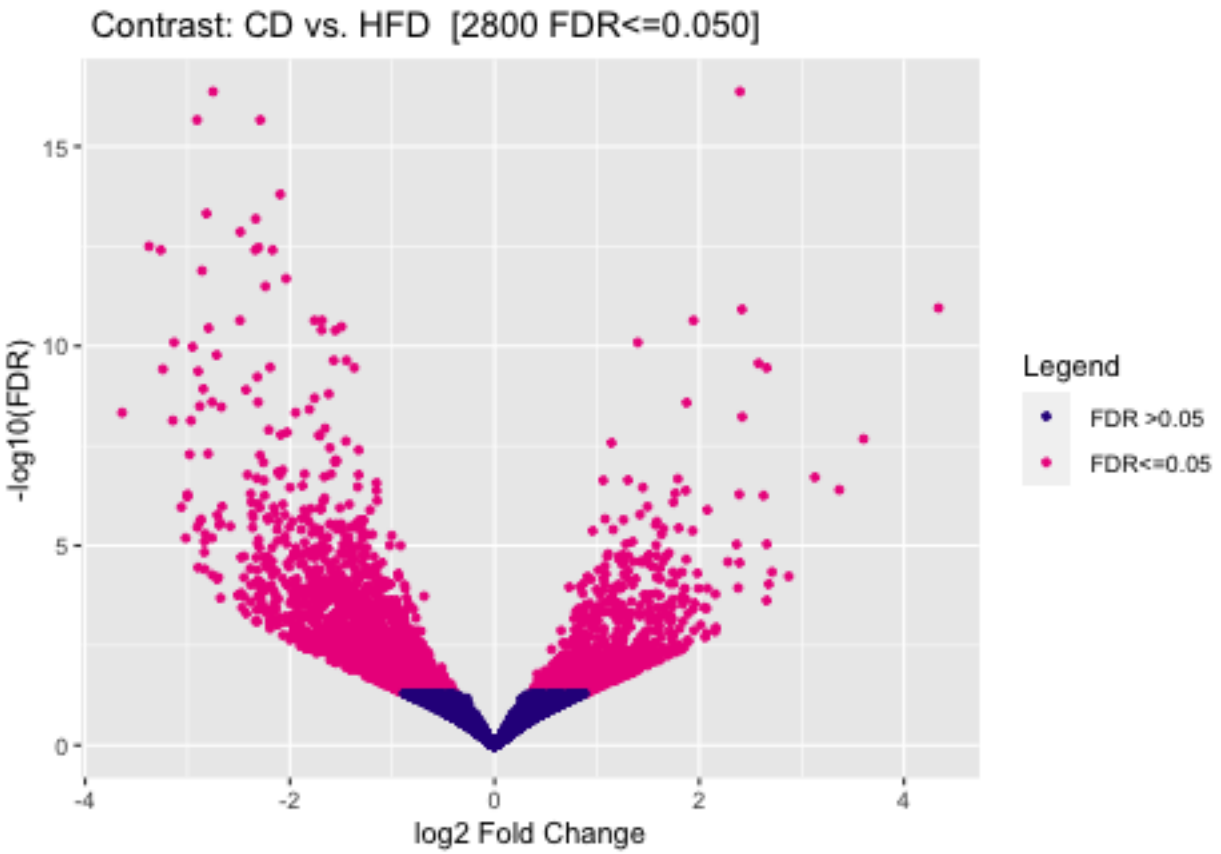
```
##       Factor Group Samples Group2 Samples2 DB.DESeq2
## 1  Treatment    CD       3    HFD        3      2800
## 2  Treatment    CD       3    DPN        3       104
## 3  Treatment    CD       3    DIP        3       227
## 4  Treatment    CD       3     E2        3       166
## 5  Treatment    CD       3    PPT        3       136
## 6  Treatment   HFD       3    DPN        3       562
```

```
## 7  Treatment   HFD       3    DIP        3        77
## 8  Treatment   HFD       3     E2        3       644
## 9  Treatment   HFD       3    PPT        3       997
## 10 Treatment   DPN       3    DIP        3         2
## 11 Treatment   DPN       3     E2        3        13
## 12 Treatment   DPN       3    PPT        3         5
## 13 Treatment   DIP       3     E2        3         1
## 14 Treatment   DIP       3    PPT        3         2
## 15 Treatment   PPT       3     E2        3         0
```

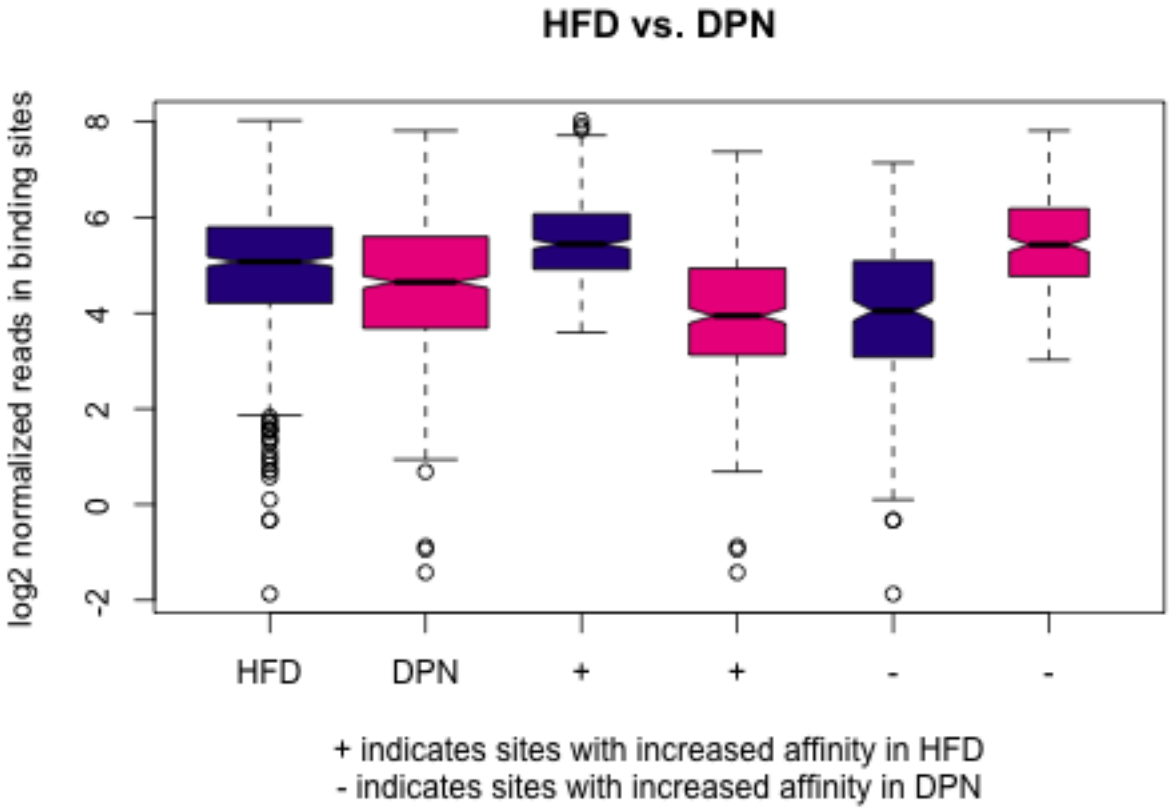
```
dba.plotPCA(samplesheet.analysed_K27, contrast = 1)
```




```
dba.plotVolcano(samplesheet.analysed_K27, contrast = 1)
```




```
dba.plotBox(samplesheet.analysed_K27, contrast =6)
```



Choose appropriate contrasts, export the full tables, then filter for signficant changes with a minimum foldchange of 50% up or down. # Then split the peaks into Loss/Gain in HFD and export bed files with these sites.

```
samplesheet.analysed_K27
```

```
## 18 Samples, 57716 sites in matrix:
##       ID  Factor Treatment Replicate    Reads FRiP
## 1    CD2 H3K27ac        CD         1 21227665 0.17
## 2    CD6 H3K27ac        CD         2 12314978 0.20
## 3    CD9 H3K27ac        CD         3 18625961 0.16
## 4   HFD3 H3K27ac       HFD         1 19237373 0.17
## 5   HFD4 H3K27ac       HFD         2 20167826 0.17
## 6   HFD6 H3K27ac       HFD         3 12831261 0.18
## 7   DPN2 H3K27ac       DPN         1 19492675 0.16
## 8   DPN3 H3K27ac       DPN         2 21083300 0.16
## 9   DPN6 H3K27ac       DPN         3 14175773 0.19
## 10  DIP3 H3K27ac       DIP         1 13121224 0.20
## 11  DIP6 H3K27ac       DIP         2 13362305 0.20
## 12 DIP10 H3K27ac       DIP         3 11599539 0.19
## 13  E2_2 H3K27ac        E2         1 14096089 0.20
## 14  E2_8 H3K27ac        E2         2 18028631 0.17
## 15  E2_9 H3K27ac        E2         3 18884119 0.16
## 16  PPT1 H3K27ac       PPT         1 11979475 0.19
## 17  PPT2 H3K27ac       PPT         2 12519231 0.18
## 18  PPT3 H3K27ac       PPT         3 12723121 0.19
##
```

```
## Design: [~Treatment] | 15 Contrasts:
##       Factor Group Samples Group2 Samples2 DB.DESeq2
## 1  Treatment    CD       3    HFD        3      2800
## 2  Treatment    CD       3    DPN        3       104
## 3  Treatment    CD       3    DIP        3       227
## 4  Treatment    CD       3     E2        3       166
## 5  Treatment    CD       3    PPT        3       136
## 6  Treatment   HFD       3    DPN        3       562
## 7  Treatment   HFD       3    DIP        3        77
## 8  Treatment   HFD       3     E2        3       644
## 9  Treatment   HFD       3    PPT        3       997
## 10 Treatment   DPN       3    DIP        3         2
## 11 Treatment   DPN       3     E2        3        13
## 12 Treatment   DPN       3    PPT        3         5
## 13 Treatment   DIP       3     E2        3         1
## 14 Treatment   DIP       3    PPT        3         2
## 15 Treatment   PPT       3     E2        3         0
```

```
res_deseq_K27_CD_vs_HFD <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contras
res_deseq_K27_HFD_vs_DPN <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contra
res_deseq_K27_HFD_vs_DIP <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contra
res_deseq_K27_HFD_vs_E2 <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contras
res_deseq_K27_HFD_vs_PPT <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contra
res_deseq_K27_DPN_vs_DIP <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contra
res_deseq_K27_DPN_vs_E2 <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contras
res_deseq_K27_DPN_vs_PPT <- as.data.frame(dba.report(samplesheet.analysed_K27, method=DBA_DESEQ2, contra

# Just too see how many different peaks are identified amongst the treatments. We wont need these peaks
nrow(res_deseq_K27_DPN_vs_DIP %>% dplyr::filter(FDR< 0.05 & abs(Fold) > 0.585))
```

```
## [1] 2
```

```
nrow(res_deseq_K27_DPN_vs_E2 %>% dplyr::filter(FDR< 0.05 & abs(Fold) > 0.585))
```

```
## [1] 13
```

```
nrow(res_deseq_K27_DPN_vs_PPT %>% dplyr::filter(FDR< 0.05 & abs(Fold) > 0.585))
```

```
## [1] 4
```

```
Diffbind_tables <- list()
Diffbind_tables$unfiltered <- list(K27_CDvsHFD = res_deseq_K27_CD_vs_HFD,
                                   K27_HFDvsDPN = res_deseq_K27_HFD_vs_DPN,
                                   K27_HFDvsE2 = res_deseq_K27_HFD_vs_E2,
                                   K27_HFDvsPPT = res_deseq_K27_HFD_vs_PPT)

Diffbind_tables$all_DB_peaks <- list()
Diffbind_tables$up_DB_peaks <- list()
Diffbind_tables$down_DB_peaks <- list()

Diffbind_bed_files <- list(
```

```
  all_DB_peaks=list(),
  up_DB_peaks=list(),
  down_DB_peaks=list())
# This loop saves the diffbound peaks in the diffbind_tables list
# This loop also saves the bedfiles in a separate list

for (i in 1:length(Diffbind_tables$unfiltered)) {

  ### PART 1 - Put the up- and downregulated peak objects (in the given contrast orientations) into data
  #Both up-and downregulated together
  Diffbind_tables$all_DB_peaks[[i]] <- Diffbind_tables$unfiltered[[i]] %>% dplyr::filter(FDR< 0.05 & abs
  #Only the upregulated peaks
  Diffbind_tables$up_DB_peaks[[i]] <- Diffbind_tables$unfiltered[[i]] %>% dplyr::filter(FDR< 0.05 & Fold
  #Only the downregulated peaks
  Diffbind_tables$down_DB_peaks[[i]] <- Diffbind_tables$unfiltered[[i]] %>% dplyr::filter(FDR< 0.05 & Fo

  ### PART 2 - Convert the objects to bedgraph format.
  Diffbind_bed_files$all_DB_peaks[[i]] <- Diffbind_tables$unfiltered[[i]] %>%
    dplyr::filter(FDR< 0.05 & abs(Fold) > 0.585) %>%
    dplyr::select(1:3) %>% mutate(name = "NA") %>% mutate(strand = "NA")

  Diffbind_bed_files$up_DB_peaks[[i]] <- Diffbind_tables$unfiltered[[i]] %>%
    dplyr::filter(FDR< 0.05 & Fold > 0.585) %>%
    dplyr::select(1:3) %>% mutate(name = "NA") %>% mutate(strand = "NA")

  Diffbind_bed_files$down_DB_peaks[[i]] <- Diffbind_tables$unfiltered[[i]] %>%
    dplyr::filter(FDR< 0.05 & Fold < -0.585) %>%
    dplyr::select(1:3) %>% mutate(name = "NA") %>% mutate(strand = "NA")
}

names(Diffbind_tables$all_DB_peaks) <- names(Diffbind_tables$unfiltered)
names(Diffbind_tables$up_DB_peaks) <- names(Diffbind_tables$unfiltered)
names(Diffbind_tables$down_DB_peaks) <- names(Diffbind_tables$unfiltered)
names(Diffbind_bed_files$all_DB_peaks) <- names(Diffbind_tables$unfiltered)
names(Diffbind_bed_files$up_DB_peaks) <- names(Diffbind_tables$unfiltered)
names(Diffbind_bed_files$down_DB_peaks) <- names(Diffbind_tables$unfiltered)

saveRDS(Diffbind_tables, "results/Epigenome_analysis/Diffbind_results_FDR_fold.rds")

# Export the bedfiles. These will be used later in the analysis.

for (i in 1:length(Diffbind_bed_files)) {

write.table(x = Diffbind_bed_files$all_DB_peaks[[i]], file=paste0("results/Epigenome_analysis/Diffbind_a
                                  names(Diffbind_bed_files$all_DB_peaks[i]),".bed"), sep="\t", quote=F, r

write.table(x = Diffbind_bed_files$up_DB_peaks[[i]], file=paste0("results/Epigenome_analysis/Diffbind_up
                                  names(Diffbind_bed_files$up_DB_peaks[i]),".bed"), sep="\t", quote=F, re

write.table(x = Diffbind_bed_files$down_DB_peaks[[i]], file=paste0("results/Epigenome_analysis/Diffbind_
                                  names(Diffbind_bed_files$down_DB_peaks[i]),".bed"), sep="\t", quote=F,
}
```

#load the packages for the annotations

```
library("ChIPpeakAnno")
library("GenomicRanges")
options(connectionObserver = NULL) #That is a work-around, as the org.Mm. package cannot be loaded
library("org.Mm.eg.db")
library("biomaRt")
```

#Annotate all of the coordinates of DiffBound peaks in the different objects. Nearest gene.

```
# For annotation, we use the September 2019 version, which was also used for RNAseq.
listEnsemblArchives()
```

```
##              name     date                                 url version
## 1  Ensembl GRCh37 Feb 2014          https://grch37.ensembl.org  GRCh37
## 2     Ensembl 110 Jul 2023 https://jul2023.archive.ensembl.org     110
## 3     Ensembl 109 Feb 2023 https://feb2023.archive.ensembl.org     109
## 4     Ensembl 108 Oct 2022 https://oct2022.archive.ensembl.org     108
## 5     Ensembl 107 Jul 2022 https://jul2022.archive.ensembl.org     107
## 6     Ensembl 106 Apr 2022 https://apr2022.archive.ensembl.org     106
## 7     Ensembl 105 Dec 2021 https://dec2021.archive.ensembl.org     105
## 8     Ensembl 104 May 2021 https://may2021.archive.ensembl.org     104
## 9     Ensembl 103 Feb 2021 https://feb2021.archive.ensembl.org     103
## 10    Ensembl 102 Nov 2020 https://nov2020.archive.ensembl.org     102
## 11    Ensembl 101 Aug 2020 https://aug2020.archive.ensembl.org     101
## 12    Ensembl 100 Apr 2020 https://apr2020.archive.ensembl.org     100
## 13     Ensembl 99 Jan 2020 https://jan2020.archive.ensembl.org      99
## 14     Ensembl 98 Sep 2019 https://sep2019.archive.ensembl.org      98
## 15     Ensembl 97 Jul 2019 https://jul2019.archive.ensembl.org      97
## 16     Ensembl 96 Apr 2019 https://apr2019.archive.ensembl.org      96
## 17     Ensembl 95 Jan 2019 https://jan2019.archive.ensembl.org      95
## 18     Ensembl 94 Oct 2018 https://oct2018.archive.ensembl.org      94
## 19     Ensembl 93 Jul 2018 https://jul2018.archive.ensembl.org      93
## 20     Ensembl 80 May 2015 https://may2015.archive.ensembl.org      80
## 21     Ensembl 77 Oct 2014 https://oct2014.archive.ensembl.org      77
## 22     Ensembl 75 Feb 2014 https://feb2014.archive.ensembl.org      75
## 23     Ensembl 54 May 2009 https://may2009.archive.ensembl.org      54
##    current_release
## 1
## 2               *
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
```

```
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23
```

```
mart <- useMart(biomart = "ensembl", dataset = "mmusculus_gene_ensembl", host = "https://sep2019.archive
# use the getAnnotation function to obtain the TSS for ensembl GRCh38.p13.
annoData <- getAnnotation(mart, featureType = "TSS")

# Annotate the peak files.
Diffbind_tables$annotated <- Diffbind_tables

for (i in 1:length(Diffbind_tables$annotated)) {
  for (k in 1:length(Diffbind_tables$annotated$unfiltered)) {

    colnames(Diffbind_tables$annotated[[i]][[k]]) <- c("chrom", "start", "end")
    nrow(Diffbind_tables$annotated[[i]][[k]])

Diffbind_tables$annotated[[i]][[k]] <- makeGRangesFromDataFrame(Diffbind_tables$annotated[[i]][[k]],
                                                                start.field = "start", end.field = "end

#Give ranges numeric names in order
names(Diffbind_tables$annotated[[i]][[k]]) <- c(1:length(Diffbind_tables$annotated[[i]][[k]]))

#Annotate granges with the nearest TSS
Diffbind_tables$annotated[[i]][[k]] <- annotatePeakInBatch(Diffbind_tables$annotated[[i]][[k]],
                               AnnotationData=annoData,
                               featureType = "TSS",
                               output="nearestLocation",
                               PeakLocForDistance = "start")

Diffbind_tables$annotated[[i]][[k]] <- as.data.frame(Diffbind_tables$annotated[[i]][[k]]) %>% remove_ro

  }
}

saveRDS(Diffbind_tables$annotated, file="results/Epigenome_analysis/Diffbind_all_annotated_DB_peaks.rds
```

```
sessionInfo()
```

```
## R version 4.2.3 (2023-03-15)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur ... 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
##
## locale:
```

```
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] biomaRt_2.54.1              org.Mm.eg.db_3.16.0
##  [3] AnnotationDbi_1.60.2        ChIPpeakAnno_3.32.0
##  [5] DiffBind_3.8.4              SummarizedExperiment_1.28.0
##  [7] Biobase_2.58.0              MatrixGenerics_1.10.0
##  [9] matrixStats_1.0.0           GenomicRanges_1.50.2
## [11] GenomeInfoDb_1.34.9         IRanges_2.32.0
## [13] S4Vectors_0.36.2            BiocGenerics_0.44.0
## [15] lubridate_1.9.2             forcats_1.0.0
## [17] stringr_1.5.0               dplyr_1.1.2
## [19] purrr_1.0.2                 readr_2.1.4
## [21] tidyr_1.3.0                 tibble_3.2.1
## [23] ggplot2_3.4.3               tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##   [1] BiocFileCache_2.6.1      plyr_1.8.8               lazyeval_0.2.2
##   [4] splines_4.2.3            BiocParallel_1.32.6      amap_0.8-19
##   [7] digest_0.6.33            ensembldb_2.22.0         invgamma_1.1
##  [10] htmltools_0.5.5          SQUAREM_2021.1           fansi_1.0.4
##  [13] magrittr_2.0.3           memoise_2.0.1            BSgenome_1.66.3
##  [16] tzdb_0.4.0               InteractionSet_1.26.1    limma_3.54.2
##  [19] Biostrings_2.66.0        annotate_1.76.0          systemPipeR_2.4.0
##  [22] bdsmatrix_1.3-6          timechange_0.2.0         prettyunits_1.1.1
##  [25] jpeg_0.1-10              colorspace_2.1-0         blob_1.2.4
##  [28] rappdirs_0.3.3           apeglm_1.20.0            ggrepel_0.9.3
##  [31] xfun_0.39                crayon_1.5.2             RCurl_1.98-1.12
##  [34] graph_1.76.0             survival_3.5-3           glue_1.6.2
##  [37] gtable_0.3.3             zlibbioc_1.44.0          XVector_0.38.0
##  [40] DelayedArray_0.24.0      scales_1.2.1             futile.options_1.0.1
##  [43] mvtnorm_1.2-2            DBI_1.1.3                Rcpp_1.0.11
##  [46] xtable_1.8-4             progress_1.2.2           emdbook_1.3.13
##  [49] bit_4.0.5                truncnorm_1.0-9          htmlwidgets_1.6.2
##  [52] httr_1.4.6               gplots_3.1.3             RColorBrewer_1.1-3
##  [55] pkgconfig_2.0.3          XML_3.99-0.14            farver_2.1.1
##  [58] dbplyr_2.3.3             deldir_1.0-9             locfit_1.5-9.8
##  [61] utf8_1.2.3               tidyselect_1.2.0         labeling_0.4.2
##  [64] rlang_1.1.1              munsell_0.5.0            tools_4.2.3
##  [67] cachem_1.0.8             cli_3.6.1                generics_0.1.3
##  [70] RSQLite_2.3.1            evaluate_0.21            fastmap_1.1.1
##  [73] yaml_2.3.7               knitr_1.43               bit64_4.0.5
##  [76] caTools_1.18.2           AnnotationFilter_1.22.0  KEGGREST_1.38.0
##  [79] RBGL_1.74.0              formatR_1.14             xml2_1.3.5
##  [82] compiler_4.2.3           rstudioapi_0.15.0        filelock_1.0.2
##  [85] curl_5.0.1               png_0.1-8                geneplotter_1.76.0
##  [88] stringi_1.7.12           highr_0.10               futile.logger_1.4.3
##  [91] GenomicFeatures_1.50.4   lattice_0.20-45          ProtGenerics_1.30.0
##  [94] Matrix_1.5-3             multtest_2.54.0          vctrs_0.6.3
##  [97] pillar_1.9.0             lifecycle_1.0.3          bitops_1.0-7
```

```
## [100] irlba_2.3.5.1            rtracklayer_1.58.0       R6_2.5.1
## [103] BiocIO_1.8.0             latticeExtra_0.6-30      hwriter_1.3.2.1
## [106] ShortRead_1.56.1         KernSmooth_2.23-20       codetools_0.2-19
## [109] lambda.r_1.2.4           MASS_7.3-58.2            gtools_3.9.4
## [112] DESeq2_1.38.3            rjson_0.2.21             withr_2.5.0
## [115] regioneR_1.30.0          GenomicAlignments_1.34.1 Rsamtools_2.14.0
## [118] GenomeInfoDbData_1.2.9   parallel_4.2.3           hms_1.1.3
## [121] VennDiagram_1.7.3        grid_4.2.3               coda_0.19-4
## [124] rmarkdown_2.23           GreyListChIP_1.30.0      ashr_2.2-54
## [127] mixsqp_0.3-48            bbmle_1.0.25             numDeriv_2016.8-1.1
## [130] interp_1.1-4             restfulr_0.0.15
```